

GenCore version 5.1.6  
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OM nucleic - protein search, using frame\_plus\_n2p model

Run on: March 18, 2004, 02:03:25 ; Search time 139.5 Seconds  
(without alignments)

12796.027 Million cell updates/sec

Title: US-09-719-272-1

Perfect score: 1138

Sequence: 1 gatccgactgaaggactcc.....atttgaataatcagattttc 3467

Scoring table:

OLIGO  
Xgapop 60.0 , Xgapext 60.0  
Ygapop 60.0 , Ygapext 60.0  
Fgapop 6.0 , Fgapext 7.0  
Delop 6.0 , Delext 7.0

Searched: 1045404 seqs, 257433775 residues

Word size: 1

Total number of hits satisfying chosen parameters: 2003896

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Listing first 45 summaries

Command line parameters:

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-DB=Published Applications AA -QFMT=fastan -SUFFIX=rapb -MINMATCH=0.1  
-LOOPCL=0 -LOOPEXT=0 -UNITS=bits -START=1 -END=1 -MATRIX=oligo  
-TRANS=human40.cdi -LIST=45 -LOCALIGN=200 -THR\_SCORE=quality -THR\_MIN=1  
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-MAXLEN=200000000 -USER=US09719272 @CGN\_1\_1\_23 @runat\_09032004\_085231\_7520  
-NCPU=6 -ICPU=3 -NO MAP -LARGESQRY -NEG SCORES=0 -WAIT -DSPBLOCK=100  
-LONGLOG -DEV TIMEOUT=120 -WAEN TIMEOUT=30 -THREADS=1 -XGAPOP=60 -XGAPEXT=60  
-FGAPOP=6 -FGAPEXT=7 -YGAPOP=60 -YGAPEXT=60 -DELOP=6 -DELEXT=7

Database : Published Applications AA:

- 1: /cgn2\_6/ptodata/1/pubpaa/US07\_PUBCOMB.pep.\*
- 2: /cgn2\_6/ptodata/1/pubpaa/PCT\_NEW\_PUB.pep.\*
- 3: /cgn2\_6/ptodata/1/pubpaa/US05\_NEW\_PUB.pep.\*
- 4: /cgn2\_6/ptodata/1/pubpaa/US06\_PUBCOMB.pep.\*
- 5: /cgn2\_6/ptodata/1/pubpaa/US07\_NEW\_PUB.pep.\*
- 6: /cgn2\_6/ptodata/1/pubpaa/PCTUS\_PUBCOMB.pep.\*
- 7: /cgn2\_6/ptodata/1/pubpaa/US08\_NEW\_PUB.pep.\*
- 8: /cgn2\_6/ptodata/1/pubpaa/US08\_PUBCOMB.pep.\*
- 9: /cgn2\_6/ptodata/1/pubpaa/US09A\_PUBCOMB.pep.\*
- 10: /cgn2\_6/ptodata/1/pubpaa/US09B\_PUBCOMB.pep.\*
- 11: /cgn2\_6/ptodata/1/pubpaa/US09C\_PUBCOMB.pep.\*
- 12: /cgn2\_6/ptodata/1/pubpaa/US09\_NEW\_PUB.pep.\*
- 13: /cgn2\_6/ptodata/1/pubpaa/US10A\_PUBCOMB.pep.\*
- 14: /cgn2\_6/ptodata/1/pubpaa/US10B\_PUBCOMB.pep.\*
- 15: /cgn2\_6/ptodata/1/pubpaa/US10C\_PUBCOMB.pep.\*
- 16: /cgn2\_6/ptodata/1/pubpaa/US10\_NEW\_PUB.pep.\*
- 17: /cgn2\_6/ptodata/1/pubpaa/US60\_NEW\_PUB.pep.\*
- 18: /cgn2\_6/ptodata/1/pubpaa/US60\_PUBCOMB.pep.\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Query Match	Length	ID	Description

1	607	53.3	647	15	US-10-291-265-722	Sequence 722, App
2	607	53.3	1907	15	US-10-291-265-250	Sequence 250, App
3	442	38.6	442	9	US-09-925-300-950	Sequence 350, App
4	296	26.0	296	14	US-10-374-539-3	Sequence 9, Appl
5	296	26.0	296	15	US-10-374-499-9	Sequence 13, Appl
6	289	25.4	289	14	US-10-314-232-13	Sequence 8, Appl
7	202	17.8	306	9	US-09-788-626-8	Sequence 21, Appl
8	197	17.3	294	9	US-09-788-626-27	Sequence 54, Appl
9	59	5.2	1502	9	US-09-808-602-54	Sequence 55, Appl
10	59	5.2	1502	10	US-09-800-198-44	Sequence 45, Appl
11	59	5.2	1948	9	US-09-808-602-55	Sequence 46, Appl
12	59	5.2	1948	10	US-09-800-198-45	Sequence 29636, A
13	55	4.9	57	14	US-10-029-386-29636	Sequence 12, Appl
14	40	3.5	1495	15	US-10-258-666-12	Sequence 38, Appl
15	34	3.0	2029	12	US-10-087-684-38	Sequence 38, Appl
16	34	3.0	2029	12	US-10-218-779-38	Sequence 39, Appl
17	34	3.0	2037	12	US-10-087-684-39	Sequence 39, Appl
18	34	3.0	2037	12	US-10-218-779-39	Sequence 191, App
19	30	2.6	162	15	US-10-334-143-191	Sequence 30320, A
20	29	2.5	64	14	US-10-029-386-30320	Sequence 21, Appl
21	20	1.8	20	14	US-10-340-288-21	Sequence 28, Appl
22	15	1.3	20	14	US-10-340-288-28	Sequence 9, Appl
23	14	1.2	176	14	US-10-314-232-9	Sequence 47, Appl
24	14	1.2	289	14	US-10-314-232-47	Sequence 11, Appl
25	14	1.2	322	14	US-10-314-232-11	Sequence 6, Appl
26	14	1.2	354	10	US-09-095-478-6	Sequence 8, Appl
27	14	1.2	379	10	US-09-095-478-8	Sequence 15, Appl
28	14	1.2	401	14	US-10-314-232-15	Sequence 1, Appl
29	14	1.2	412	10	US-09-095-478-3	Sequence 2, Appl
30	14	1.2	426	10	US-09-095-478-1	Sequence 22, Appl
31	14	1.2	463	10	US-09-095-478-2	Sequence 6, Appl
32	14	1.2	898	14	US-10-314-232-22	Sequence 2, Appl
33	14	1.2	2281	12	US-10-087-684-6	Sequence 6, Appl
34	14	1.2	2281	12	US-10-218-779-6	Sequence 2, Appl
35	14	1.2	2291	10	US-09-822-871-2	Sequence 10, Appl
36	14	1.2	2300	12	US-10-087-684-10	Sequence 10, Appl
37	14	1.2	2300	12	US-10-218-779-10	Sequence 4, Appl
38	14	1.2	2301	10	US-09-822-871-4	Sequence 37, Appl
39	14	1.2	2302	12	US-10-087-684-37	Sequence 37, Appl
40	14	1.2	2302	12	US-10-218-779-37	Sequence 25, Appl
41	12	1.1	20	14	US-10-340-288-25	Sequence 85, Appl
42	12	1.1	33	15	US-10-052-648A-85	Sequence 158623, A
43	12	1.1	56	12	US-10-424-599-158623	Sequence 323, App
44	12	1.1	98	15	US-10-074-978A-323	Sequence 95, Appl
45	12	1.1	105	12	US-10-087-684-95	

ALIGNMENTS

RESULT 1  
US-10-291-265-722  
; Sequence 722, Application US/10291265  
; Publication No. US20030232054A1  
; GENERAL INFORMATION:  
; APPLICANT: Hvaeq, Inc.  
; APPLICANT: Tang et al  
; TITLE OF INVENTION: No. US20030232054A1el Nucleic Acids and Polypeptides  
; FILE REFERENCE: 21272-017 (785)  
; CURRENT APPLICATION NUMBER: US/10/291,265  
; CURRENT FILING DATE: 2000-01-25  
; PRIOR APPLICATION NUMBER: 09/491,404  
; PRIOR FILING DATE: 2000-01-25  
; PRIOR APPLICATION NUMBER: 09/617,746  
; PRIOR FILING DATE: 2000-07-17  
; PRIOR APPLICATION NUMBER: 09/631,451  
; PRIOR FILING DATE: 2000-08-03  
; PRIOR APPLICATION NUMBER: 09/633,870  
; PRIOR FILING DATE: 2000-09-15  
; NUMBER OF SEQ ID NOS: 944  
; SOFTWARE: FastSeq for Windows Version 3.0  
; SEQ ID NO 722  
; LENGTH: 647  
; TYPE: PRT

ORGANISM: Homo sapiens  
US-10-291-265-722

Alignment Scores:  
Pred. No.: 0  
Score: 607.00  
Percent Similarity: 100.00%  
Best Local Similarity: 100.00%  
Query Match: 53.34%  
DB: 15

US-09-719-272-1 (1-3467) x US-10-291-265-722 (1-647)

QY	6	GGACTGAAGACTCTCTGTCGGCCCACTCTCTGACCTCTGAGATGGAGGCTCAAC	65
DB	41	GlyLeuLeuAspSerLeuLeuAlaHisSerSerAspProValGluMetArgLeuLeu	60
QY	66	TACACAGCCCGAGTATGCGAGACCAACCCATCCCATCACCGACCTGGCGGACAAC	125
DB	61	TyrGlnThrProGlyMetArgAspHisProProIleThrAspLeuAlaAspAsn	80
QY	126	ATCGAGCGCTCAAGCCCAACGATGGCTCAAGTTCTCCAGAGTATGATCCATCGAC	185
DB	81	IleGluArgLeuLeuAlaAsnAspGlyLeuLeuPheSerGlnGluTyrGluSerIleAsp	100
QY	186	CCTGGACAGAGTCTACGTGGAGAAATCAAACTCGAGGTGAACAAGCCCAAGACCGC	245
DB	101	ProGlyGlnGlnPheThrTrpGluLeuSerAsnLeuGluValAsnLeuProLeuAsnArg	120
QY	246	TATGCGAATGTATCGCTACGACCACTCTCGAGTCACTCTACCTCTCATCGATGGCGTC	305
DB	121	TyrAlaAsnValIleAlaTyrAspHisSerArgValIleLeuThrSerIleAspGlyVal	140
QY	306	CCCGGAGTGAATCAATCAATGCAATCATCATGATGGCTACCGCAAGCAGAAATGCTAC	365
DB	141	ProGlySerAspTyrIleAsnAlaAsnTyrIleAspGlyTyrArgGlyGlnAsnAlaTyr	160
QY	366	ATGCCACGAGGCGCCCTGCGGAGACCATGGCGATTTCTGGAGATGGTGGGAA	425
DB	161	IleAlaThrGlnGlyProLeuProGluThrMetGlyAspPheTrpArgMetValTrpGlu	180
QY	426	CACGACGCGCCACTGTGGTCAATGATGACACGCGCTGGAGGAGAGTCCCGGTAAATGT	485
DB	181	GlnArgThrAlaThrValValMetMetThrArgLeuGluGluLeuSerArgValLeu	200
QY	486	GATCAGTACTGGCCAGCCCGTGGACGACGACTGTGGCCCTTATTCAGGTGACCTGTG	545
DB	201	AspGlnTyrTrpProAlaArgGlyThrGluThrCysGlyLeuIleGlnValThrLeuLeu	220
QY	546	GACACAGTGGAGTGGCCCATACACTGTGGCCACCTTCGCACTCCACAGAGTGGCTCC	605
DB	221	AspThrValGluLeuAlaThrTyrThrValArgThrPheAlaLeuHisLysSerGlySer	240
QY	606	AGTGAGAAGCGTCAAGTGGCTCAGTTTCAGTTTCATGGCCCTGGCCAGACCATGAGTTCT	665
DB	241	SerGluLeuArgGluLeuArgGlnPheGlnPheMetAlaTrpProAspHisGlyValPro	260
QY	666	GAGTACCCAACTCCCACTCGCTTCTTACGACGCGGTCAAGCCCTGCAACCCCTAGAC	725
DB	261	GluTyrProThrProIleLeuAlaPheLeuArgArgValLysAlaCysAsnProLeuAsp	280
QY	726	GCAGGCGCCCATGTGGTGCATCTACGCGCGGGTGGCGCGCCGCTCTCATCGTG	785
DB	281	AlaGlyProMetValValHisCysSerAlaGlyValGlyArgThrGlyCysPheIleVal	300
QY	786	ATTGATGCCATGTGGAGCGGATGAACAGACGAGACGCGTGACATCTATGGCCACGTG	845
DB	301	IleAspAlaMetLeuGluArgMetLysHisGluLeuThrValAspIleTyrGlyHisVal	320
QY	846	ACCTGATGCGATCAGAGGAACTACATGGTGGACGAGGACGACGATCGTTTCATC	905
DB	321	ThrCysMetArgSerGlnArgAsnTyrMetValGlnThrGluAspGlnTyrValPheIle	340

QY	906	CATGAGCGCTGCTGAGGCTGCCAGCTGGCGCCACACAGAGGTGCTGCTCCCGCAACCTG	965
DB	341	HisGluAlaLeuLeuGluAlaAlaThrCysGlyHisThrGluValProAlaArgHisLeu	360
QY	966	TATGCCCATCCAGAAAGCTGGGCCAAGTGCCTCCAGGGAGAGTGTGACCCCATGGAG	1025
DB	361	TyrAlaHisIleGlnLysLeuGlyGlnValProProGlyGluSerValThrAlaMetGlu	380
QY	1026	CTCGAGTTCAAGTCTGCTGGCAGCTCCAGGCCACACGCTCCCGCTTCATCAGCCCAAC	1085
DB	381	LeuGluPheLysLeuLeuAlaSerSerLysAlaHisThrSerArgPheIleSerAlaAsn	400
QY	1086	CTGCCCTGCAACAAGTTCAAGAACCGCTGGTGAACATCATCCCTACCAATTTGACCGT	1145
DB	401	LeuProCysAsnLysPheLysAsnArgLeuValAsnIleMetProTyrGluLeuThrArg	420
QY	1146	GTGTGCTGCACCCCATCCGTGTGTGGAGGCTCTGACTACATCAATCCAGCTTCCTG	1205
DB	421	ValCysLeuGlnProIleArgGlyValGluGlySerAspTyrIleAsnAlaSerPheLeu	440
QY	1206	GATGTTATAGACAGCAGAGGCTTACATAGCTACACAGGGGCTTGGCAGAGGACCC	1265
DB	441	AspGlyTyrArgGlnGlnLysAlaTyrIleAlaThrGlnGlyProLeuAlaGluSerThr	460
QY	1266	GAGGACTTCTGGCGCATGCTATGGAGCACAATTCACCACATCATGCTATGCTGACCAAG	1325
DB	461	GluAspPheTrpArgMetLeuTrpGluHisAsnSerThrIleValMetLeuThrLys	480
QY	1326	CTTCGGAGATGGGAGGAGAAATGCCACCACTACTGGCCAGCAGAGCGCTCTGCTCGC	1385
DB	481	LeuArgGluMetGlyArgGluLysCysHisGlnTyrTrpProAlaGluArgSerAlaArg	500
QY	1386	TACCACTACTTTTGTGTGACCCGATGGCTGAGTACACATGCCAGTATATCTCGCT	1445
DB	501	TyrGlnTyrPheValValAspProMetAlaGluTyrAsnMetProGlnTyrIleLeuArg	520
QY	1446	GAGTTCAAGCTCACGAGTCCCGGATGGGAGTGGCAGTCAAGACCAATCCGGCAGTTCCAGTTC	1505
DB	521	GluPheLysValThrAspAlaArgAspGlyGlnSerArgThrIleArgGlnPheGlnPhe	540
QY	1506	ACAGACTGCCACAGAGCGGCTGCCAAGACAGCGGAGGATTCATTGACTTCATCGGG	1565
DB	541	ThrAspTrpProGluGlnGlyValProLysThrGlyGluGlyPheIleAspPheIleGly	560
QY	1566	CAGGTGCATAACCAAGGAGCAGTTGGACAGGATGGCCATCACGCTGACATGTCAGT	1625
DB	561	GlnValHisLysThrLysGlnPheGlyGlnAspGlyProIleThrValHisCysSer	580
QY	1626	GCTGGCGTGGCGCCACCGGGTGTTCATCACTCTGAGCATGCTCTCGAGCGCATGCGC	1685
DB	581	AlaGlyValGlyArgThrGlyValPheIleThrLeuSerIleValLeuGluArgMetArg	600
QY	1686	TATGAGGCGTGGTGCACATGTTTCAGACCGTGAAGACCCCTCGGTACACAGCGTCTGCG	1745
DB	601	TyrGluGlyValValAspMetPheGlnThrValLysThrLeuArgThrGlnArgProAla	620
QY	1746	ATGCTGCACACAGAGCCAGTATCAGCTGCTGCTACCGTGGCGCCCTGAGTACCTCGGC	1805
DB	621	MetValGlnThrGluAspGlnTyrGlnLeuCysTyrArgAlaAlaLeuGluTyrLeuGly	640
QY	1806	AGCTTTGACCACTATGCCAACG	1826
DB	641	SerPheAspHisTyrAlaThr	647

RESULT 2

US-10-291-265-250  
; Sequence 250, Application US/10291265  
; Publication No. US20030232054A1  
; GENERAL INFORMATION:  
; APPLICANT: Hyseq, Inc.  
; APPLICANT: Tang et al  
; TITLE OF INVENTION: No. US20030232054A1 Nucleic Acids and Polypeptides  
; FILE REFERENCE: 21272-017 (785)

; CURRENT APPLICATION NUMBER: US/10/291,265  
; CURRENT FILING DATE: 2000-01-25  
; PRIOR APPLICATION NUMBER: 09/491,404  
; PRIOR FILING DATE: 2000-01-25  
; PRIOR APPLICATION NUMBER: 09/617,746  
; PRIOR FILING DATE: 2000-07-17  
; PRIOR APPLICATION NUMBER: 09/631,451  
; PRIOR FILING DATE: 2000-08-03  
; PRIOR APPLICATION NUMBER: 09/633,870  
; PRIOR FILING DATE: 2000-09-15  
; NUMBER OF SEQ ID NOS: 944  
; SOFTWARE: FastSeq for Windows Version 3.0  
; SEQ ID NO 250  
; LENGTH: 1907  
; TYPE: PRT  
; ORGANISM: Homo sapiens  
US-10-291-265-250

Alignment Scores:  
Pred. No.: 0 Length: 1907  
Score: 607.00 Matches: 607  
Percent Similarity: 100.00% Conservative: 0  
Best Local Similarity: 100.00% Mismatches: 0  
Query Match: 53.34% Indels: 0  
DB: 15 Gaps: 0

US-09-719-272-1 (1-3467) x US-10-291-265-250 (1-1907)

Qy	6	GGACTGAAGGACTCTTGTCTGGCCCACTCTCTGACCCCTGTGGAGATGCGGAGGCTCAAC	65
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Qy	66	TACAGACCCAGGTATGCGAGACACACCCACCCATCCCATCACCGACCTGGCGGCAAC	125
Db	1321	TyrGlnThrProGlyMetArgAspHisProProileProleThrAspLeuAlaAspAsn	1340
Qy	126	ATCCAGGCGCTCAAGCCCAAGGCTCAAGTCTCCAGAGGATGATGATCCATCGAC	185
Db	1341	IleGluArgLeuLysAlaAsnAspGlyLeuLysPheSerGlnGlyThrGlySerIleAsp	1360
Qy	186	CTTGACAGCAGGATTCACGTGGGAGAAATTCAAACCTGGAGGTGAACAAGCCCAAGCCGC	245
Db	1361	ProGlyGlnGlnPheThrTrpGluAsnSerAsnLeuGluValAsnLysProLysAsnArg	1380
Qy	246	TATCGGAATGTCATCGCTAGACACATCTCGAGTATCCTTACTCTATCGATGGGCTC	305
Db	1381	TyrAlaAsnValIleAlaTyAspHisSerArgValIleLeuThrSerIleAspGlyVal	1400
Qy	306	CCGGGAGTGACTACATCAATGCCAATCTACATCGATCGCTACCGCAAGCAGAAATGCTTAC	365
Db	1401	ProGlySerAspTyrIleAlaAlaAsnTrpIleAspGlyTyrArgLysGlnAsnAlaTyr	1420
Qy	366	ATCGCCACGCGAGGCCCCCTGCGGAGACCATGCGGCGATTTCTGGAGAATGGTGGGAA	425
Db	1421	IleAlaThrGlnGlyProLeuProGluThrMetGlyAspPheTrpArgMetValTrpGlu	1440
Qy	426	CAGCGCAGCGGCATGTGTGTCATGATGACAGCGCTGGAGGAGAGTCCCGGGTAAATGT	485
Db	1441	GlnArgThrAlaThrValValMetMetThrArgLeuGluLysSerArgValLysCys	1460
Qy	486	GATCAGTACTGGCGCCGCGGACCGAGACCTGTGCGCTTATTCAGGTGACCTGCTTG	545
Db	1461	AspGlnTyrTrpProAlaArgGlyThrGluThrCysGlyLeuIleGlnValThrLeuLeu	1480
Qy	546	GACACAGTGGAGCTGGCCACATACATGTGTGGCACCTTCGCACCTCCACAAAGATGGCTCC	605
Db	1481	AspThrValGluLeuAlaThrTyrThrValArgThrPheAlaLeuHisLysSerGlySer	1500
Qy	606	AGTGAGAAGCGTGAGCTGCGTCAATTTCAGTTTCATGGCTGGCCAGACCATGAGGTTCTCT	665
Db	1501	SerGluLysArgGluLeuArgGlnPheGlnPheMetAlaTrpProAspHisGlyValPro	1520
Qy	666	GAGTACCACCACTCCATCTGGCCTTCTCAGCAGCGGTCAAGGCTGCAACCCCTAGAC	725

Db	1521	GluTyrProThrProIleLeuAlaPheLeuArgArgValLysAlaCysAsnProLeuAsp	1540
Qy	726	GCAGGGCCCATGTGTGTCACATGTCAGCGCGGGGTGGCCGCCACCGCTCTTCATCGTG	785
Db	1541	AlaGlyProMetValValHisCysSerAlaGlyValGlyArgThrGlyCysPheIleVal	1560
Qy	786	ATTGATCCCATGTGTGGAGCGGATGAAGCAGAGACGGTGGACATCTATGGCCACGTG	845
Db	1561	IleAspAlaMetLeuGluArgMetLysHisGluLysThrValAspIleTyrGlyHisVal	1580
Qy	846	ACCTGTCATGTCATCACAGAGCAATACATGTCGACAGCAGGACCACTAGTCTTCATC	905
Db	1581	ThrCysMetArgSerGlnArgAsnTyrMetValGlnThrGluAspGlnTyrValPheIle	1600
Qy	906	CATGAGCGCTGTGGAGGCTGCCACGTGCGGCACACAGAGGTGCTGCCGCCAACCTG	965
Db	1601	HisGluAlaLeuLeuGluAlaAlaThrCysGlyHisThrGluValProAlaArgAsnLeu	1620
Qy	966	TATGCCCATCCAGAGCTGGGCCAGTCCCTCCAGGGGAGAGTGTGACCGCATCGAG	1025
Db	1621	TyrAlaHisIleGlnLysLeuGlyGlnValProProGlyGluSerValThrAlaMetGlu	1640
Qy	1026	CTCGAGTTCAGTTCCTGGCCAGCTCCCAAGGCCACACAGTCCCGCTTCATCAGCGCCAAC	1085
Db	1641	LeuGluPheLysLeuLeuAlaSerSerLysAlaHisThrSerArgPheIleSerAlaAsn	1660
Qy	1086	CTGCCCTGCAACAGTTCAAGAACCCGGCTGGTGAACATCATGCCCTACGATTCACCGT	1145
Db	1661	LeuProCysAsnLysPheLysAsnArgLeuValAsnIleMetProTyrGluLeuThrArg	1680
Qy	1146	GTGTGTCGAGCCCATCCGTGTGTGGAGGCTCTGACTACATCATTCAGTTCAGTTCCTG	1205
Db	1681	ValCysLeuGlnProIleArgGlyValGluGlySerAspTyrIleAsnAlaSerPheLeu	1700
Qy	1206	GATGTTTATAGACAGCAGAGGCTTACATAGCTACACAGGGGCTCTGGCAGAGAGCACC	1265
Db	1701	AspGlyTyrArgGlnGlnLysAlaTyrIleAlaThrGlnGlyProLeuAlaGluSerThr	1720
Qy	1266	GAGGACTCTTGGCGCATGTCTATGGAGCACAATTCACCATCATCTGTCATGCTGACCAAG	1325
Db	1721	GluAspPheTrpArgMetLeuTrpGluHisAsnSerThrIleValMetLeuThrLys	1740
Qy	1326	CTTGGGAGATGGCGGAGGAGAAATGCCACCTACTTGGCCAGCAGAGCGCTCTGCTCGC	1385
Db	1741	LeuArgGluMetGlyArgGluLysCysHisGlnTyrTrpProAlaGluArgSerAlaArg	1760
Qy	1386	TACCAGTACTTGTGTGTGACCCGATGGCTGAGTACAAACATGCCCACTATATCTCTCGT	1445
Db	1761	TyrGlnTyrPheValValAspProMetAlaGluTyrAsnMetProGlnTyrIleLeuArg	1780
Qy	1446	GAGTTCAGGTCAAGGATGCCCGGATGGCAGTCAAGGACAAATCCGGCAGTTCACAGTTC	1505
Db	1781	GluPheLysValThrAspAlaArgAspGlyGlnSerArgThrIleArgGlnPheGlnPhe	1800
Qy	1506	ACAGACTGGCCAGCAGGCGCTGCCACAGCAGGCGGAGGATTCATTGACTTCATCGGG	1565
Db	1801	ThrAspTrpProGluGlnGlyValProLysThrGlyGlyPheIleAspPheIleGly	1820
Qy	1566	CAGTGTCAATGAAGACCAAGGAGCAGTTTGGACAGATGGGCTTATCAGCGTGCACTGAGT	1625
Db	1821	GlnValHisLysThrLysGluGlnPheGlyGlnAspGlyProIleThrValHisCysSer	1840
Qy	1626	GCTGGCGTGGCCGACCGGGGTGTTTCATCCTGAGCATCTCTCTGGAGCGCATGCGC	1685
Db	1841	AlaGlyValGlyArgThrGlyValPheIleThrLeuSerIleValLeuGluArgMetArg	1860
Qy	1686	TATGAGGCGGTGTGCACATGTTTCAGACCGTGAAGACCTCGGTACACAGCGTCTGCCC	1745
Db	1861	TyrGluGlyValValAspMetPheGlnThrValLysThrLeuArgThrGlnArgProAla	1880
Qy	1746	ATCGTGCAGACAGCAGCAGTATCAGTCTGCTACCGTGGCGCCCTGGAGTACCTCGGC	1805

Db 1881 MetValGlnThrGluAspGlnTyrGlnLeuCysTyrArgAlaAlaLeuGluTyrLeuGly 1900  
QY 1806 AGCTTTGACCACTATGCAACG 1826  
Db 1901 SerPheAspHisTyrAlaThr 1907  
RESULT 3  
US-09-925-300-950  
; Sequence 950, Application US/09925300  
; Patent No. US20020151681A1  
; GENERAL INFORMATION:  
; APPLICANT: Craig Ruben,  
; APPLICANT: Steve Ruben  
; TITLE OF INVENTION: Nucleic Acids, Proteins and Antibodies  
; FILE REFERENCE: PA101  
; CURRENT APPLICATION NUMBER: US/09/925,300  
; CURRENT FILING DATE: 2001-08-10  
; PRIOR APPLICATION NUMBER: PCT/US00/05988  
; PRIOR FILING DATE: 2000-03-08  
; PRIOR APPLICATION NUMBER: 60/124,270  
; PRIOR FILING DATE: 1999-03-12  
; NUMBER OF SEQ ID NOS: 1890  
; SOFTWARE: Patentin Ver. 2.0  
; SEQ ID NO 950  
; LENGTH: 442  
; TYPE: PRT  
; ORGANISM: Homo sapiens  
US-09-925-300-950  
Alignment Scores:  
Pred. No.: 0 Length: 442  
Score: 442.00 Matches: 442  
Percent Similarity: 100.00% Conservative: 0  
Best Local Similarity: 100.00% Mismatches: 0  
Query Match: 38.84% Indels: 0  
DB: 9 Gaps: 0  
US-09-719-272-1 (1-3467) x US-09-925-300-950 (1-442)  
QY 501 GCCCGTGGCAGCAGACCTGTGGCTTATTCAGGTCAACCTGTGTGACACAGTGGAGCTG 560  
Db 1 AlaArgGlyThrGluThrCysGlyLeuIleGlnValThrLeuLeuAspThrValGluLeu 20  
QY 561 GCCACATACATGTGGGACCTTGGCCTCCACAGAGTGGCTCCAGTGAGAGCGTGAG 620  
Db 21 AlaThrTyrThrValArgThrPheAlaLeuHisLysSerGlySerGluLysArgGlu 40  
QY 621 CTGCGTCACTTCAGTTCATGGCTGGCCAGACCATGGAGTTCCTCAGTACCACTCCC 680  
Db 41 LeuArgGlnPheGlnPheMetAlaTrpProAspHisGlyValProGluTyrProThrPro 60  
QY 681 ATCTCTGGCTTCTTACGACGGGTCAAGGCTGCAACCCCTAGACGAGGCGCCATGGTG 740  
Db 61 IleLeuAlaPheLeuArgArgValLysAlaCysAsnProLeuAspAlaGlyProMetVal 80  
QY 741 GTGCATGACGCGCGGCTGGGCCCGCCAGCGGTCTTTCATCGTATTGATGTCATGGTG 800  
Db 81 ValHisCysSerAlaGlyValGlyArgThrGlyCysPheIleValIleAspAlaMetLeu 100  
QY 801 GAGCGGATGAAGCAGCAGAGCGGTGGACATCTATGGCCACGTGACCTGCGATCGCATCA 860  
Db 101 GluArgMetLysHisGlyThrValAspIleTyrGlyHisValThrCysMetArgSer 120  
QY 861 CAGAGAACTACATGTGACAGCGGAGGACCACTAGTGTTCATCATCAGGCGGTGCTG 920  
Db 121 GlnArgAsnTyrMetValGlnThrGluAspGlnTyrValPheIleHisGluAlaLeuLeu 140  
QY 921 GAGGCTGCCACGTGGCGGCCACACAGAGTGCCTGCCCGCACTGATGCCCACTCCAG 980  
Db 141 GluAlaAlaThrCysGlyHisThrGluValProAlaArgAsnLeuTyrAlaHisIleGln 160  
QY 981 AAGCTGGGCCAGTGTCTCCAGGGGAGGTGTACCGCCATGGAGCTCGAGTTCAGATTG 1040

Db 161 LysLeuGlyGlnValProProGlyGluSerValThrAlaMetGluLeuGluPheLysLeu 180  
QY 1041 CTGGCCAGCTCTCAAGGCCCCACACGCTCCCGCTTTCATCAGCGCAACCTCCCTCGCAACAG 1100  
Db 181 LeuAlaSerSerLysAlaHisThrSerArgPheIleSerAlaAsnLeuProCysAsnLys 200  
QY 1101 TTCAGAACCGGCTGGTGAACATCATGCGCTACGAATGACCCCGTGTCTGTCGAGGCC 1160  
Db 201 PheLysAsnArgLeuValAsnIleMetProTyrGluLeuThrArgValCysLeuGlnPro 220  
QY 1161 ATCCGTGTGTGGAGGGCTCTGACTACATCAATCAATCCAGCTCTCTCGATGGTTATAGACAG 1220  
Db 221 IleArgGlyValGluGlySerAspTyrIleAsnAlaSerPheLeuAspGlyTyrArgGln 240  
QY 1221 CAGAGGCTACATAGCTACACAGGGCTCTGGCAGAGAGCAGCAGAGACTTCTGGCGC 1280  
Db 241 GlnLysAlaTyrIleAlaThrGlnGlyProLeuAlaGluSerThrGluAspPheTrpArg 260  
QY 1281 ATGCTATGGAGCACAATCCACCACATCATGTCATGCTGACCAAGCTTCGGGAGAGTGGC 1340  
Db 261 MetLeuTrpGluHisAsnSerThrIleIleValMetLeuThrLysLeuArgGluMetGly 280  
QY 1341 AGGGAGAAATGCCACCACTACTGGCCAGCAGAGCGCTCTGCTCGCTACCAAGTACTTGT 1400  
Db 281 ArgGluLysCysHisGlnTyrTrpProAlaGluArgSerAlaArgTyrGlnTyrPheVal 300  
QY 1401 GTTGACCCGATGGCTGAGTACAAATGCCACAGTATATCTCTGCGTGAAGTTCAGGTCAAG 1460  
Db 301 ValAspProMetAlaGluTyrAsnMetProGlnTyrIleLeuArgGluPheLysValThr 320  
QY 1461 GATGCCCGGATGGGCACTCAAGGACAATCCGGCAGTTCAGTTCACAGACTGGCCAGAG 1520  
Db 321 AspAlaArgAspGlyGlnSerArgThrIleArgGlnPheGlnPheThrAspTrpProGlu 340  
QY 1521 CAGGGCGTCCCAACACAGAGGGAGGATTTCATTGACTTTCATCGGCGAGGTGCATAGACC 1580  
Db 341 GlnGlyValProLysThrGlyGluGlyPheIleAspPheIleGlnValHisLysThr 360  
QY 1581 AAGGAGAGTTTGGACAGGATGGGCTTATCAGGTGCACTGCGGTGCGGTGGCGTGGCGCCG 1640  
Db 361 LysGluGlnPheGlyGlnAspGlyProIleThrValHisCysSerAlaGlyValGlyArg 380  
QY 1641 ACCGGGTGTTCATCCTCAGCATCTGAGCATCTCTGGAGCGCATCGCTATGAGGCGGTGGTC 1700  
Db 381 ThrGlyValPheIleThrLeuSerIleValLeuGluArgMetArgTyrGluGlyValVal 400  
QY 1701 GACATGTTTTCAGACCGTGAAGACCCCTGCGTACACAGCGTCTCTGCCATGTCGAGACAG 1760  
Db 401 AspMetPheGlnThrValLysThrLeuArgThrGlnArgProAlaMetValGlnThrGlu 420  
QY 1761 GACAGTATCAGCTGTGCTACCGTGGCGCCCTGGAGTACCTCGGAGCTTTGACCACTAT 1820  
Db 421 AspGlnTyrGlnLeuCysTyrArgAlaAlaLeuGluTyrLeuGlySerPheAspHisTyr 440  
QY 1821 GCAACG 1826  
Db 441 AlaThr 442  
RESULT 4  
US-10-374-539-3  
; Sequence 3, Application US/10374539  
; Publication No. US20030195247A1  
; GENERAL INFORMATION:  
; APPLICANT: SUNESIS PHARMACEUTICALS, INC.  
; APPLICANT: BARR, Kenneth  
; APPLICANT: FAHR, Bruce  
; APPLICANT: HANSEN, Stig  
; APPLICANT: MCDOWELL, Robert  
; APPLICANT: WIESMAN, Chris  
; APPLICANT: ZHU, Jian  
; TITLE OF INVENTION: COMPOUNDS THAT MODULATE THE ACTIVITY OF  
; TITLE OF INVENTION: PTP-1B AND TC-PTP  
; FILE REFERENCE: 39750-0008

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; CURRENT APPLICATION NUMBER: US/10/374,539
; CURRENT FILING DATE: 2003-02-25
; PRIOR APPLICATION NUMBER: US 60/361,475
; PRIOR FILING DATE: 2002-03-01
; NUMBER OF SEQ ID NOS: 29
; SOFTWARE: FAST-SEQ for Windows Version 4.0
; SEQ ID NO 3
; LENGTH: 296
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-374-539-3

Alignment Scores:
Pred. No.: 6,38e-260 Length: 296
Score: 296.00 Matches: 296
Percent Similarity: 100.00% Conservative: 0
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 26.01% Indels: 0
DB: 14 Gaps: 0

US-09-719-272-1 (1-3467) x US-10-374-539-3 (1-296)
QY 102 CCATCAGGAGTATGATGCTTCCATGAGGCGCTCAAAGCCAAAGCTGAGTGGCTCAAGTTC 161
DB 1 ProlileThrAspLeuAlaAspAsnIleGluArgLeuLysAlaAsnAspGlyLeuLysPhe 20
QY 162 TCCAGGAGTATGATGCTTCCATGAGGCGCTCAAAGCCAAAGCTGAGTGGCTCAAGTTC 221
DB 21 SerGlnGluTyrGluSerIleAspProGlyGlnGlnPheThrTrpGluAsnSerAsnLeu 40
QY 222 GAGGTGAACAGCCAGACCGGTATCGCATGCTCCGCTACGACCGCTCCGCTACGACCGCT 281
DB 41 GluValAsnLysProllysAsnArgTyrAlaAsnValIleAlaTyrAspHisSerArgVal 60
QY 282 ATCCTTACCTTATCGATGCGTCCCGGAGTGACTACATCAATGCAACTACATCGAT 341
DB 61 IleLeuThrSerIleAspGlyValProGlySerAspTyrIleAsnAlaAsnTyrIleAsp 80
QY 342 GAGTGAACAGCCAGACCGGTATCGCATGCTCCGCTACGACCGCTCCGCTACGACCGCT 401
DB 101 AspPheTrpArgMetValTrpGluGlnArgThrAlaThrValValMetMetThrArgLeu 120
QY 462 GAGGAGAGTCCCGGTAAATGTGATCTAGTACTGGCCAGCCCGCTGGCAGCAGCTGT 521
DB 121 GluGluLysSerArgValLysCysAspGlnTyrTrpProAlaArgGlyThrGluThrCys 140
QY 522 GGCCTTATTCAGTGACCCCTGTTGGAACAGCGACCGCCACTGTGTCATGATGACGCGCTG 581
DB 141 GlyLeuIleGlnValThrLeuAspThrValGluLeuAlaThrTyrThrValArgThr 160
QY 582 TTGCGACTCCACAGAGTGGCTCCAGTGAGAGCGGTGAGTGGCTGAGTGGCTGAGTGGCT 641
DB 161 PheAlaLeuHisLysSerGlySerGlySerGlySerGlySerGlySerGlySerGlySer 180
QY 642 GCCTGGCCAGACCATGAGTTCCTGAGTACCCAACTCCCTGCGCTCCCTGCGCTCCCTG 701
DB 181 AlaTrpProAspHisGlyValProGluTyrProThrProlleLeuAlaPheLeuArgArg 200
QY 702 GTCAGGCGCTGCAACCCCTAGACGAGGCGCCATGCTGTCATGCTGTCATGCTGTCATG 761
DB 201 ValLysAlaCysAsnProLeuAspAlaGlyProMetValValHisCysSerAlaGlyVal 220
QY 762 GCGCGCACCGGCTGCTTCATGCTGATGATGCTGATGCTGATGCTGATGCTGATGCTG 821
DB 221 GlyArgThrGlyCysPheIleValIleAspAlaMetLeuGluArgMetLysHisGluLys 240
QY 822 ACCGTGACATCTATGATGCTGATGCTGATGCTGATGCTGATGCTGATGCTGATGCTG 881
DB 241 ThrValAspIleTyrGlyHisValThrCysMetArgSerGlnArgAsnTyrMetValGln 260

; CURRENT APPLICATION NUMBER: US/10/374,499
; CURRENT FILING DATE: 2003-02-25
; PRIOR APPLICATION NUMBER: US 60/377,034
; PRIOR FILING DATE: 2002-05-01
; NUMBER OF SEQ ID NOS: 9
; SOFTWARE: FAST-SEQ for Windows Version 4.0
; SEQ ID NO 9
; LENGTH: 296
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-374-499-9

GENERAL INFORMATION:
; APPLICANT: SUNESIS PHARMACEUTICALS, INC.
; APPLICANT: ERLANSON, Daniel A.
; APPLICANT: MCDOWELL, Robert S.
; TITLE OF INVENTION: METHODS FOR IDENTIFYING COMPOUNDS THAT
; TITLE OF INVENTION: MODULATE ENZYMAIC ACTIVITY
; FILE REFERENCE: 39750-0016
; CURRENT APPLICATION NUMBER: US/10/374,499
; CURRENT FILING DATE: 2003-02-25
; PRIOR APPLICATION NUMBER: US 60/377,034
; PRIOR FILING DATE: 2002-05-01
; PRIOR APPLICATION NUMBER: US 10/121,216
; PRIOR FILING DATE: 2002-04-10
; NUMBER OF SEQ ID NOS: 9
; SOFTWARE: FAST-SEQ for Windows Version 4.0
; SEQ ID NO 9
; LENGTH: 296
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-374-499-9

Alignment Scores:
Pred. No.: 6,38e-260 Length: 296
Score: 296.00 Matches: 296
Percent Similarity: 100.00% Conservative: 0
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 26.01% Indels: 0
DB: 15 Gaps: 0

US-09-719-272-1 (1-3467) x US-10-374-499-9 (1-296)
QY 102 CCATCAGGAGTATGATGCTTCCATGAGGCGCTCAAAGCCAAAGCTGAGTGGCTCAAGTTC 161
DB 1 ProlileThrAspLeuAlaAspAsnIleGluArgLeuLysAlaAsnAspGlyLeuLysPhe 20
QY 162 TCCAGGAGTATGATGCTTCCATGAGGCGCTCAAAGCCAAAGCTGAGTGGCTCAAGTTC 221
DB 21 SerGlnGluTyrGluSerIleAspProGlyGlnGlnPheThrTrpGluAsnSerAsnLeu 40
QY 222 GAGGTGAACAGCCAGACCGGTATCGCATGCTCCGCTACGACCGCTCCGCTACGACCGCT 281
DB 41 GluValAsnLysProllysAsnArgTyrAlaAsnValIleAlaTyrAspHisSerArgVal 60
QY 282 ATCCTTACCTTATCGATGCGTCCCGGAGTGACTACATCAATGCAACTACATCGAT 341
DB 61 IleLeuThrSerIleAspGlyValProGlySerAspTyrIleAsnAlaAsnTyrIleAsp 80
QY 342 GAGTGAACAGCCAGACCGGTATCGCATGCTCCGCTACGACCGCTCCGCTACGACCGCT 401
DB 81 GlyTyrArgLysGlnAsnAlaTyrIleAlaThrGlnGlnPheThrTrpGluAsnSerAsnLeu 100
QY 402 GAGTGAACAGCCAGACCGGTATCGCATGCTCCGCTACGACCGCTCCGCTACGACCGCT 461
DB 101 AspPheTrpArgMetValTrpGluGlnArgThrAlaThrValValMetMetThrArgLeu 120
QY 462 GAGGAGAGTCCCGGTAAATGTGATCTAGTACTGGCCAGCCCGCTGGCAGCAGCTGT 521
DB 121 GluGluLysSerArgValLysCysAspGlnTyrTrpProAlaArgGlyThrGluThrCys 140
QY 522 GGCCTTATTCAGTGACCCCTGTTGGAACAGCGACCGCCACTGTGTCATGATGACGCGCTG 581
DB 141 GlyLeuIleGlnValThrLeuAspThrValGluLeuAlaThrTyrThrValArgThr 160
QY 582 TTGCGACTCCACAGAGTGGCTCCAGTGAGAGCGGTGAGTGGCTGAGTGGCTGAGTGGCT 641
DB 161 PheAlaLeuHisLysSerGlySerGlySerGlySerGlySerGlySerGlySerGlySer 180
QY 642 GCCTGGCCAGACCATGAGTTCCTGAGTACCCAACTCCCTGCGCTCCCTGCGCTCCCTG 701
DB 181 AlaTrpProAspHisGlyValProGluTyrProThrProlleLeuAlaPheLeuArgArg 200
QY 702 GTCAGGCGCTGCAACCCCTAGACGAGGCGCCATGCTGTCATGCTGTCATGCTGTCATG 761
DB 201 ValLysAlaCysAsnProLeuAspAlaGlyProMetValValHisCysSerAlaGlyVal 220
QY 762 GCGCGCACCGGCTGCTTCATGCTGATGATGCTGATGCTGATGCTGATGCTGATGCTG 821
DB 221 GlyArgThrGlyCysPheIleValIleAspAlaMetLeuGluArgMetLysHisGluLys 240
QY 822 ACCGTGACATCTATGATGCTGATGCTGATGCTGATGCTGATGCTGATGCTGATGCTG 881
DB 241 ThrValAspIleTyrGlyHisValThrCysMetArgSerGlnArgAsnTyrMetValGln 260
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; ORGANISM: Homo sapiens
US-09-788-626-8

Alignment Scores:
Pred. No.: 2,11e-174 Length: 306
Score: 202.00 Matches: 250
Percent Similarity: 97.66% Conservative: 0
Best Local Similarity: 97.66% Mismatches: 0
Query Match: 17.75% Indels: 6
DB: 9 Gaps: 0

US-09-719-272-1 (1-3467) x US-09-788-626-8 (1-306)
QY 195 CAGTTACGTGGAGATTCACAACTGGAGTGAACAGCCCAAGAACCGCTATGCAAT 254
Db 1 GlnPheThrTrpGluAsnSerAsnLeuGluValAsnLysProLysAsnArgTyrAlaAsn 20
QY 255 GTCATCGCTTACCACTCTCGAGTCATCTTACCTCTATCATCGCGTCCCGGAGT 314
Db 21 ValIleAlaTyrAspHisSerArgValIleLeuThrSerIleAspGlyValProGlySer 40
QY 315 GACTACATCAATCCCACTACATCGATGGTACCGCAAGCAGAAATGCTTACATCGCCACG 374
Db 41 AspTyrIleAsnAlaAsnTyrIleAspGlyTyrArgLysGlnAsnAlaTyrIleAlaThr 60
QY 375 CAGGGCCCTGCGCAGACCATGGCGATTTCTGGAGATGCTGTGGNAACAGCGCAG 434
Db 61 GlnGlyProLeuProGluThrMetGlyAspPheTrpArgMetValTrpGluGlnArgThr 80
QY 435 GCCACTGTGTGATGATGACACCGCTGGAGGAGAAGTCCCGGTAATAATGTGATCAGTAC 494
Db 81 AlaThrValValMetMetThrArgLeuGluGluLysSerArgValLysCysAspGlnTyr 100
QY 495 TGCCACGCCCGTGGCCAGACCTGTGGCTTATTACAGTGACCTGTGGACACAGTG 554
Db 101 TrpProAlaArgGlyThrGluThrCysGlyLeuIleGlnValThrLeuLeuAspThrVal 120
QY 555 GAGCTGGCCACATACACTGTGGCCACTTGCCTCCACCAAGAGTGGCTCCAGTGAGAAG 614
Db 121 GluLeuAlaThrTyrThrVal-----PheAlaLeuHisLysSerGlySerGluLys 138
QY 615 CGTGAGCTGCTCAGTTTTCAGTTTCATGCGCTGCCACAGCATGGAGTTCTCGAGTACCCA 674
Db 139 ArgGluLeuArgGlnPheGlnPheMetAlaTrpProAspHisGlyValProGluTyrPro 158
QY 675 ACTCCCATCTGCTCTTCTACGACCGGTCAAGCTTCAACCCCTAGACGCGGCCCC 734
Db 159 ThrProIleLeuAlaPheLeuArgValLysAlaCysAsnProLeuAspAlaGlyPro 178
QY 735 ATGGTGTGCACTGACGCGCGGCGTGGCGCGCACCGGCTGCTTCATCGTATTGATGCC 794
Db 179 MetValValHisCysSerAlaGlyValGlyArgThrGlyCysPheIleValIleAspAla 198
QY 795 ATGTTGGAGCGGATGAAGCACGAGAACGCTGGACATCTATGGCCACGCTGACCTGCATG 854
Db 199 MetLeuGluArgMetLysHisGluLysThrValAspIleTyrGlyHisValThrCysMet 218
QY 855 CGATCAGAGGAACTACATGTTGTCAGACGAGGAGCAGTACGTGTTTCATCCATGAGGG 914
Db 219 ArgSerGlnArgAsnTyrMetValGlnThrGluAspGlnTyrValPheIleHisGluAla 238
QY 915 CTGCTGGAGGCTCCACGCTGGCGCCACACAGAGGTG 950
Db 239 LeuLeuGluAlaAlaThrCysGlyHisThrGluVal 250

RESULT 8
US-09-788-626-27
; Sequence 27, Application US/09788626
; Patent No. US2002009762A1
; GENERAL INFORMATION:
; APPLICANT: Flint, Andrew J.
; APPLICANT: Cool, Deborah E.
; TITLE OF INVENTION: IMPROVED ASSAY FOR PROTEIN TYROSINE
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; TITLE OF INVENTION: PHOSPHATES
; FILE REFERENCE: 200125.401
; CURRENT APPLICATION NUMBER: US/09/788,626
; CURRENT FILING DATE: 2001-02-13
; NUMBER OF SEQ ID NOS: 40
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 27
; LENGTH: 294
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-788-626-27

Alignment Scores:
Pred. No.: 7,5e-170 Length: 294
Score: 197.00 Matches: 245
Percent Similarity: 97.61% Conservative: 0
Best Local Similarity: 97.61% Mismatches: 0
Query Match: 17.31% Indels: 6
DB: 9 Gaps: 0

US-09-719-272-1 (1-3467) x US-09-788-626-27 (1-294)
QY 1062 ACGTCCCGCTTCATCAGCGCCCAACCTGCCCTCCAAACAAGTTCAAGAACCGGTGTGAAC 1121
Db 1 ThrSerArgPheIleSerAlaAsnLeuProCysAsnLysPheLysAsnArgLeuValAsn 20
QY 1122 ATCATGCCCTACGAATTGACCCGCTGTGTCTGTCAGAGCCCATCGTGGTGTGAGGGCTCT 1181
Db 21 IleMetProTyrGluLeuThrArgValCysLeuGlnProIleArgGlyValGluGlySer 40
QY 1182 GACTACATCAATGCCAGCTTCTCGATGGTGTATAGACAGCAGAACGCCCTACATAGTACA 1241
Db 41 AspTyrIleAsnAlaSerPheLeuAspGlyTyrArgGlnGlnLysAlaTyrIleAlaThr 60
QY 1242 CAGGGGCCCTCTGGCAGAGACACCGAGGACTTCTGGCGCATCTATGGGAGCACAAATCC 1301
Db 61 GlnGlyProLeuAlaGluSerThrGluAspPheTrpArgMetLeuTrpGluHisAsnSer 80
QY 1302 ACATCATCTCATCTGACCAAGCTTCGGAGATGGGAGGAGGAGAAATGCCACCAAGTAC 1361
Db 81 ThrIleValMetLeuThrLysLeuArgGluMetGlyArgGluLysCysHisGlnTyr 100
QY 1362 TGGCCAGCAGAGCGCTCTGCTCGCTACCAAGTACTTGTGTGTGACCCGATGGCTGAGTAC 1421
Db 101 TrpProAlaGluArgSerAlaArgTyrGlnTyrPheValValAspProMetAlaGluTyr 120
QY 1422 AACATGCCCCAGTATATCTGCTGAGTTCAAAGTCAACGATGCCCGGATGGGCAAGTCA 1481
Db 121 AsnMetProGlnTyrIleLeu-----PheLysValThrAspAlaAspGlyGlnSer 138
QY 1482 AGGACAAATCCGCGAGTTCAGTTTCAGACTGGCCAGAGCAGGCGTGCACAGACAGC 1541
Db 139 ArgThrIleArgGlnPheGlnPheThrAspTyrProGluGlnGlyValProLysThrGly 158
QY 1542 GAGGATTCATTGACTTCATCCGGCAGGTGCATAAGACCAAGCAGCAGTTCGACAGAGAT 1601
Db 159 GluGlyPheIleAspPheIleGlnValHisLysThrLysGluGlnPheGlyGlnAsp 178
QY 1602 GGGCTTATCAGGTGCATGTCAGTGTGGCGTGGCGCCGACCGGGGTGTTCATCACTCTG 1661
Db 179 GlyProIleThrValHisCysSerAlaGlyValGlyArgThrGlyValPheIleThrLeu 198
QY 1662 AGCATCGTCTGGAGCGCATGCGCTATGAGGCGGTGCTGACATGTTTCAGACCGGTGAAG 1721
Db 199 SerIleValLeuGluArgMetArgTyrGluGlyValValAspMetPheGlnThrValLys 218
QY 1722 ACCCTGCGTACACAGCGTCTCTGCCATGGTGCAGACAGAGGACAGTATCAGTGTGCTAC 1781
Db 219 ThrLeuArgThrGlnArgProAlaMetValGlnThrGluAspGlnTyrGlnLeuCysTyr 238
QY 1782 CGTGGCGCCCTCGAGTACCTC 1802
Db 239 ArgAlaAlaLeuGluTyrLeu 245
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RESULT 9
US-09-808-602-54
; Sequence 54, Application US/09808602
; Patent No. US20020155115A1
; GENERAL INFORMATION:
; APPLICANT: Vernet, Corine A
; APPLICANT: Fernandes, Elma
; APPLICANT: Shimkets, Richard A
; APPLICANT: Herrmann, John L
; APPLICANT: Majumder, Kumud
; APPLICANT: Mishra, Vishnu
; APPLICANT: Mezes, Peter S
; APPLICANT: MacDougall, John
; TITLE OF INVENTION: NOVEL PROTEINS AND NUCLEIC ACIDS ENCODING SAME
; FILE REFERENCE: 15966-697 CIP
; CURRENT APPLICATION NUMBER: US/09/808,602
; CURRENT FILING DATE: 2001-03-14
; PRIOR FILING DATE: 2001-03-05
; PRIOR APPLICATION NUMBER: 60/186,596
; PRIOR FILING DATE: 2000-03-03
; NUMBER OF SEQ ID NOS: 114
; SOFTWARE: Patentin Ver. 2.1
; SEQ ID NO 54
; LENGTH: 1502
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-808-602-54

Alignment Scores:
Pred. No.: 2,14e-44 Length: 1502
Score: 59.00 Matches: 59
Percent Similarity: 100.00% Conservative: 0
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 5.18% Indels: 0
DB: 9 Gaps: 0

US-09-719-272-1 (1-3467) x US-09-808-602-54 (1-1502)
QY 1311 GTCATGCTGACCAAGCTTCGGGAGATGGCGAGAGAAATGCCACGAGTACTGGCCAGCA 1370
DB 1331 ValMetLeuThrLysLeuArgGluMetGlyArgGluLysCysHisGlnTyrTrpProAla 1350
QY 1371 GAGCGCTCTGCTCGCTACCAAGTACTTTGTTGTGACCCGATGGCTGAGTACAACATGCC 1430
DB 1351 GluArgSerAlaArgTyrGlnTyrPheValValAspProMetAlaGluTyrAsnMetPro 1370
QY 1431 CAGTATATCTCGTGGTCAAGTCAAGTCACCGATGCCGGATGGCGAGTCAAGGACA 1487
DB 1371 GlnTyrIleLeuArgGluPheLysValThrAspAlaArgAspGlyGlnSerArgThr 1389

RESULT 10
US-09-808-198-44
; Sequence 44, Application US/09800198
; Publication No. US20030087816A1
; GENERAL INFORMATION:
; APPLICANT: Vernet, Corine AM
; APPLICANT: Fernandes, Elma
; APPLICANT: Shimkets, Richard A
; APPLICANT: Herrmann, John L
; APPLICANT: Majumder, Kumud
; APPLICANT: Mishra, Vishnu
; APPLICANT: Mezes, Peter S
; APPLICANT: Rastelli, Luca
; TITLE OF INVENTION: NOVEL PROTEINS AND NUCLEIC ACIDS ENCODING SAME
; FILE REFERENCE: 15966-697
; CURRENT APPLICATION NUMBER: US/09/800,198
; CURRENT FILING DATE: 2001-03-05
; PRIOR FILING DATE: 2000-03-03
; NUMBER OF SEQ ID NOS: 98
; SOFTWARE: Patentin Ver. 2.1
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; SEQ ID NO 44
; LENGTH: 1502
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-808-198-44

Alignment Scores:
Pred. No.: 2,14e-44 Length: 1502
Score: 59.00 Matches: 59
Percent Similarity: 100.00% Conservative: 0
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 5.18% Indels: 0
DB: 10 Gaps: 0

US-09-719-272-1 (1-3467) x US-09-808-198-44 (1-1502)
QY 1311 GTCATGCTGACCAAGCTTCGGGAGATGGCGAGAGAAATGCCACGAGTACTGGCCAGCA 1370
DB 1331 ValMetLeuThrLysLeuArgGluMetGlyArgGluLysCysHisGlnTyrTrpProAla 1350
QY 1371 GAGCGCTCTGCTCGCTACCAAGTACTTTGTTGTGACCCGATGGCTGAGTACAACATGCC 1430
DB 1351 GluArgSerAlaArgTyrGlnTyrPheValValAspProMetAlaGluTyrAsnMetPro 1370
QY 1431 CAGTATATCTCGTGGTCAAGTCAAGTCACCGATGCCGGATGGCGAGTCAAGGACA 1487
DB 1371 GlnTyrIleLeuArgGluPheLysValThrAspAlaArgAspGlyGlnSerArgThr 1389

RESULT 11
US-09-808-602-55
; Sequence 55, Application US/09808602
; Patent No. US20020155115A1
; GENERAL INFORMATION:
; APPLICANT: Vernet, Corine A
; APPLICANT: Fernandes, Elma
; APPLICANT: Shimkets, Richard A
; APPLICANT: Herrmann, John L
; APPLICANT: Majumder, Kumud
; APPLICANT: Mishra, Vishnu
; APPLICANT: Mezes, Peter S
; APPLICANT: MacDougall, John
; TITLE OF INVENTION: NOVEL PROTEINS AND NUCLEIC ACIDS ENCODING SAME
; FILE REFERENCE: 15966-697 CIP
; CURRENT APPLICATION NUMBER: US/09/808,602
; CURRENT FILING DATE: 2001-03-14
; PRIOR FILING DATE: 2001-03-05
; PRIOR APPLICATION NUMBER: 60/186,596
; PRIOR FILING DATE: 2000-03-03
; NUMBER OF SEQ ID NOS: 114
; SOFTWARE: Patentin Ver. 2.1
; SEQ ID NO 55
; LENGTH: 1948
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-808-602-55

Alignment Scores:
Pred. No.: 2,07e-44 Length: 1948
Score: 59.00 Matches: 59
Percent Similarity: 100.00% Conservative: 0
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 5.18% Indels: 0
DB: 9 Gaps: 0

US-09-719-272-1 (1-3467) x US-09-808-602-55 (1-1948)
QY 1311 GTCATGCTGACCAAGCTTCGGGAGATGGCGAGAGAAATGCCACGAGTACTGGCCAGCA 1370
DB 1777 ValMetLeuThrLysLeuArgGluMetGlyArgGluLysCysHisGlnTyrTrpProAla 1796
QY 1371 GAGCGCTCTGCTCGCTACCAAGTACTTTGTTGTGACCCGATGGCTGAGTACAACATGCC 1430
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Db      1797  GluArgSerAlaArgTyrGlnTyrPheValValAspProMetAlaGluTyrAsnMetPro 1816
Qy      1431  CAGTATCTCTGCTGAGTTCAAGGTCAAGGATCCCGGGATGGGCAAGTCAAGGACA 1487
Db      1817  GlnTyrIleLeuArgGluPheLeuValThrAspAlaArgAepGlyGlnSerArgThr 1835

RESULT 12
US-09-800-198-45
; Sequence 45, Application US/09800198
; Publication No. US20030087816A1
; GENERAL INFORMATION:
; APPLICANT: Vernet, Cornie AM
; APPLICANT: Fernandes, Elma
; APPLICANT: Shimkets, Richard A
; APPLICANT: Herrmann, John L
; APPLICANT: Majumder, Kumud
; APPLICANT: Mishra, Vishna
; APPLICANT: Mezes, Peter S
; APPLICANT: Rastelli, Luca
; TITLE OF INVENTION: NOVEL PROTEINS AND NUCLEIC ACIDS ENCODING SAME
; FILE REFERENCE: 15966-697
; CURRENT APPLICATION NUMBER: US/09/800,198
; CURRENT FILING DATE: 2001-03-05
; PRIOR APPLICATION NUMBER: 60/186,596
; PRIOR FILING DATE: 2000-03-03
; NUMBER OF SEQ ID NOS: 98
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 45
; LENGTH: 1948
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-800-198-45

Alignment Scores:
Pred. No.:      2,07e-44      Length:      1948
Score:          59.00        Matches:      59
Percent Similarity: 100.00%    Conservative: 0
Best Local Similarity: 100.00%  Mismatches: 0
Query Match:    5.18%        Indels:      0
DB:             1.0         Gaps:        0

US-09-719-272-1 (1-3467) x US-09-800-198-45 (1-1948)

Qy      1311  GTCAATGTACCAAGCTTCGGAGATGGCAGGAGAGAAATGCCACCAAGTACTGCCAGCA 1370
Db      1777  ValMetLeuThrLysLeuArgGluMetGlyArgGluLysCysHisGlnTyrTrpProAla 1796
Qy      1371  GAGCGCTCTGCTCGCTACCAAGTACTTTGTTGTTGACCCGATGGCTGAGTACCAATGCC 1430
Db      1797  GluArgSerAlaArgTyrGlnTyrPheValValAspProMetAlaGluTyrAsnMetPro 1816
Qy      1431  CAGTATCTCTGCTGAGTTCAAGGTCAAGGATCCCGGGATGGGCAAGTCAAGGACA 1487
Db      1817  GlnTyrIleLeuArgGluPheLeuValThrAspAlaArgAepGlyGlnSerArgThr 1835

RESULT 13
US-10-029-386-29636
; Sequence 29636, Application US/10029386
; Publication No. US20030194704A1
; GENERAL INFORMATION:
; APPLICANT: Penn, Sharon G.
; APPLICANT: Rank, David R.
; APPLICANT: Hanzel, David K.
; TITLE OF INVENTION: HUMAN GENOME-DERIVED SINGLE EXON NUCLEIC ACID PROBES USEFUL FOR C
; FILE REFERENCE: AEOMICA-X-2
; CURRENT APPLICATION NUMBER: US/10/029,386
; CURRENT FILING DATE: 2001-12-20
; NUMBER OF SEQ ID NOS: 34288
; SOFTWARE: Annomax Sequence Listing Engine vers. 1.1
; SEQ ID NO 29636
; LENGTH: 57
; TYPE: PRT
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; ORGANISM: Homo sapiens
; FEATURE:
; OTHER INFORMATION: MAP TO AC011772.3
; OTHER INFORMATION: EXPRESSED IN ADULT LIVER, SIGNAL = 1.9
; OTHER INFORMATION: EXPRESSED IN FETAL LIVER, SIGNAL = 1.4
; OTHER INFORMATION: EXPRESSED IN PLACENTA, SIGNAL = 8.5
; OTHER INFORMATION: EXPRESSED IN HELA, SIGNAL = 1.4
; OTHER INFORMATION: EXPRESSED IN BRAIN, SIGNAL = 1.4
; OTHER INFORMATION: EXPRESSED IN HEART, SIGNAL = 1.2
; OTHER INFORMATION: EXPRESSED IN BONE MARROW, SIGNAL = 0.95
; OTHER INFORMATION: SWISSPROT HIT: O00470, EVALUE 1.20e+00
US-10-029-386-29636

Alignment Scores:
Pred. No.:      1,46e-40      Length:      57
Score:          55.00        Matches:      55
Percent Similarity: 100.00%    Conservative: 0
Best Local Similarity: 100.00%  Mismatches: 0
Query Match:    4.86%        Indels:      0
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US-09-719-272-1 (1-3467) x US-10-029-386-29636 (1-57)

Qy      476  CCGGAGCTTCTCCTCCAGCGGTGTCTCATCATGACACAGTGGCGCTGCTTCCACAC 417
Db      3    ProGlyLeuLeuLeuGlnProCysHisHisAspHisSerGlyArgAlaLeuPheProHis 22
Qy      416  CATTCTCCAGAAATCCCCATGCTCTCGGCGACGGGGCCCTCGTGGCGATGAGGATT 357
Db      23  HisSerProGluIleAlaHisGlyLeuGlyGlnGlyAlaLeuArgGlyAepValGlyIle 42
Qy      356  CTGCTTGGCGTAGCCATCGATGCTAGTGGCATGTAGTCACT 312
Db      43  LeuLeuAlaValAlaIleAepValValGlyIleAepValValThr 57

RESULT 14
US-10-258-666-12
; Sequence 12, Application US/10258666
; Publication No. US20040005578A1
; GENERAL INFORMATION:
; APPLICANT: Yamada, Yoji
; APPLICANT: Sekine, Susumu
; APPLICANT: Kikuchi, Yasuhiro
; APPLICANT: Sakurada, Kazuhiro
; APPLICANT: Kyowa Hakko Kogyo Co., Ltd.
; TITLE OF INVENTION: Myocardial Cell Proliferation-Associated Genes
; FILE REFERENCE: 082382-000000US
; CURRENT APPLICATION NUMBER: US/10/258,666
; CURRENT FILING DATE: 2003-05-23
; PRIOR APPLICATION NUMBER: JP 2000-126741
; PRIOR FILING DATE: 2000-04-27
; PRIOR APPLICATION NUMBER: WO PCT/JP01/03700
; PRIOR FILING DATE: 2001-04-27
; NUMBER OF SEQ ID NOS: 42
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 12
; LENGTH: 1495
; TYPE: PRT
; ORGANISM: Rattus norvegicus
; FEATURE:
; OTHER INFORMATION: RHDH-231, PTP-P1
US-10-258-666-12

Alignment Scores:
Pred. No.:      4,14e-27      Length:      1495
Score:          40.00        Matches:      40
Percent Similarity: 100.00%    Conservative: 0
Best Local Similarity: 100.00%  Mismatches: 0
Query Match:    3.51%        Indels:      0
DB:             15         Gaps:        0

US-09-719-272-1 (1-3467) x US-10-258-666-12 (1-1495)
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QY		
1327	ValMetLeuThrLysLeuArgGluMetGlyArgGluIysCysHisGIntYrTTPProAla	1346
Db		
1371	GAGCGCTCTGCTCGCTACCAAGTACTTTGTTGTTGTTGACCCGATGGCTGAGTACAACATGCCCC	1430
QY		
1347	GluArgSerAlaArgTyrGIntYrPheValValAspProMetAlaGIntYrAsnMetPro	1366
Db		

Db	1934	GlyGluGlyPheIleAspPheIleGlyGlnValHisLysThrIysGluGlnPheGlyGln	1953
Qy	1599	GATGGGCTATCACGGTCACCTGCAGTGTGGCGTGGGGCCGC	1640
Db	1954	AspGlyProIleThrValHisCysSerAlaGlyValGlyArg	1967

Search completed: March 18, 2004, 02:12:17  
Job time : 177.5 secs

RESULT	15
US-10-087-684-38	
/ Sequence 38, Application US/10087684	
/ Publication NO. US20040029116A1	
/ GENERAL INFORMATION:	
/ APPLICANT: Edinger, Shlomit R.	
/ APPLICANT: MacDougall, John R.	
/ APPLICANT: Millet, Isabelle	
/ APPLICANT: Ellerman, Karen	
/ APPLICANT: Stone, David J.	
/ APPLICANT: Grosse, William M.	
/ APPLICANT: Lepley, Denise M.	
/ APPLICANT: Rieger, Daniel K.	
/ APPLICANT: Burgess, Catherine E.	
/ APPLICANT: Casman, Stacie, J.	
/ APPLICANT: Spytek, Kimberly A.	
/ APPLICANT: Boldog, Ferenc L.	
/ APPLICANT: Li, Li	
/ APPLICANT: Padigaru, Muralidhara	
/ APPLICANT: Mishra, Vishnu	
/ APPLICANT: Shenoy, Suresh G.	
/ APPLICANT: Rastelli, Luca	
/ APPLICANT: Tchernev, Velizar T.	
/ APPLICANT: Vernet, Corine A.M.	
/ APPLICANT: Zerhusen, Bryan D.	
/ APPLICANT: Malyankar, Uriel M.	
/ APPLICANT: Guo Xiaojia	
/ APPLICANT: Miller, Charles E.	
/ APPLICANT: Gangolli, Essha A.	
/ TITLE OF INVENTION: PROTEINS AND	
/ FILE REFERENCE: 21402-214 CIP	
/ CURRENT APPLICATION NUMBER: US/10/087,684	
/ CURRENT FILING DATE: 2003-03-10	
/ PRIOR APPLICATION NUMBER: 60/253,834	
/ PRIOR FILING DATE: 2000-11-29	
/ PRIOR APPLICATION NUMBER: 60/250,926	
/ PRIOR FILING DATE: 2000-11-30	
/ PRIOR APPLICATION NUMBER: 60/264,180	
/ PRIOR FILING DATE: 2001-01-25	
/ PRIOR APPLICATION NUMBER: 60/274,194	
/ PRIOR FILING DATE: 2001-03-08	
/ PRIOR APPLICATION NUMBER: 60/313,656	
/ PRIOR FILING DATE: 2001-08-20	
/ PRIOR APPLICATION NUMBER: 60/327,456	
/ PRIOR FILING DATE: 2001-10-05	
/ NUMBER OF SEQ ID NOS: 220	
/ SOFTWARE: CuraSeqList version 0.1	
/ SEQ ID NO 38	
/ LENGTH: 2929	
/ TYPE: PRT	
/ ORGANISM: Drosophila melanogaster	
US-10-087-684-38	

Alignment Scores:		1.14e-21	2029
Pred. No.:	Score:	34.00	34
Percent Similarity:		100.00%	0
Best Local Similarity:		100.00%	0
Query Match:		2.99%	0
DB:		12	0
	Length:		
	Matches:		34
	Conservative:		0
	Mismatches:		0
	Indels:		0
	Gaps:		0

US-09-719-272-1 (1-3467) x US-10-087-684-38 (1-2029)  
OV 1539 GCGGAGGATTCATTGACTTCATCGGCGAGGTGCATTAAGACCAAGGACGAGTTTGGACAG 1598